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SV  X63673.1
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DT  21-FEB-1992 (Rel. 31, Created)
DT  19-JUL-1993 (Rel. 36, Last updated, Version 12)
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DE  C.histolyticum closI gene for alpha-clostripain
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KW  closI gene; Clostripain.
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OS  Clostridium histolyticum
OC  Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC  Clostridium.
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RA  Diefenthal T.;
RT  ;
RL  Submitted (28-JAN-1992) to the EMBL/GenBank/DDBJ databases.
RL  T. Diefenthal, Weissheimer Research, Dept. Biotechnology, Schaarstr.1,
RL  P.O.B. 20 65, W-5470 Andernach, FRG
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RN  [2]
RP  1-2368
RX  DOI; 10.1007/BF00276893
RX  MEDLINE; 93341452.
RX  PUBMED; 8341259.
RA  Dargatz H., Diefenthal T., Witte V., Reipen G., von Wettstein D.;
RT  "The heterodimeric protease clostripain from Clostridium histolyticum is
RT  encoded by a single gene";
RL  Mol. Gen. Genet. 240(1):140-145(1993).
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Entry information

Entry name **CLOS_CLOHI**
Primary accession number **P09870**
Secondary accession number **P09869**
Entered in Swiss-Prot in **Release 10, March 1989**
Sequence was last modified in **Release 26, July 1993**
Annotations were last modified in **Release 45, October 2004**

Name and origin of the protein

Protein name **Alpha-clostripain [Precursor]**
Synonyms **EC 3.4.22.8**
Clostridiopeptidase B
Gene name **Name: cloSI**
From **Clostridium histolyticum [TaxID: 1498]**
Taxonomy **Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.**

References

[1] NUCLEOTIDE SEQUENCE.

MEDLINE=93341452;PubMed=8341259 [NCBI, ExPASy, EBI, Israel, Japan]
Dargatz H., Diefenthal T., Witte V., Reipen G., von Wettstein D.;
"The heterodimeric protease clostripain from Clostridium histolyticum is encoded by a single gene.";
Mol. Gen. Genet. 240:140-145(1993).

[2] PROTEIN SEQUENCE OF 51-181.

MEDLINE=85076641;PubMed=6391922 [NCBI, ExPASy, EBI, Israel, Japan]
Gilles A.M., Lecroisey A., Keil B.;
"Primary structure of alpha-clostripain light chain.";
Eur. J. Biochem. 145:469-476(1984).

[3] PRELIMINARY PROTEIN SEQUENCE OF 51-73 AND 191-232.

MEDLINE=83131688;PubMed=6337850 [NCBI, ExPASy, EBI, Israel, Japan]
Gilles A.M., de Wolf A., Keil B.;

"Amino-acid sequences of the active-site sulfhydryl peptide and other thiol peptides from the cysteine proteinase alpha-clostripain."; Eur. J. Biochem. 130:473-479(1983).

Comments

- **FUNCTION:** Cysteine endopeptidase with strict specificity.
- **CATALYTIC ACTIVITY:** Preferential cleavage: Arg-|-Xaa, including Arg-|-Pro bond, but not Lys-|-Xaa.
- **SUBUNIT:** Heterodimer of a light chain and an heavy chain held together by strong noncovalent forces rather than by intramolecular disulfide bridges.
- **SIMILARITY:** Belongs to the peptidase C11 family [view classification].
- **DATABASE:** NAME=Worthington enzyme manual; WWW="http://www.worthington-biochem.com/CP/".

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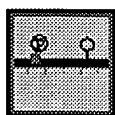
Cross-references

EMBL	X63673; CAA45212.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	A29174; A29174.
PIR	A29175; A29175.
	B29175; B29175.
	S35190; S35190.
MEROPS	C11.001; -.
InterPro	IPR005077; Peptidase_C11.
	Graphical view of domain structure.
Pfam	PF03415; Peptidase_C11; 1.
	Pfam graphical view of domain structure.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P09870.
ProtoNet	P09870.
ProtoMap	P09870.
PRESAGE	P09870.
DIP	P09870.
ModBase	P09870.
SMR	P09870; E151372FF6C95BE7.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

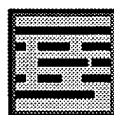
Keywords

Direct protein sequencing; Hydrolase; Signal; Thiol protease; Zymogen.

Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description
SIGNAL	1	27	27	Potential.

PROPEP	28	50	23	Potential.
CHAIN	51	181	131	Alpha-clostripain light chain.
PEPTIDE	182	190	9	Linker.
CHAIN	191	526	336	Alpha-clostripain heavy chain.
ACT_SITE	231	231		
CONFLICT	127	127		R -> NQL (in Ref. 2).
CONFLICT	176	179		HGGG -> GDGH (in Ref. 2).
CONFLICT	197	197		S -> H (in Ref. 3).
CONFLICT	213	213		I -> L (in Ref. 3).
CONFLICT	216	216		H -> T (in Ref. 3).
CONFLICT	232	232		L -> M (in Ref. 3).

Sequence information

Length: **526 AA** [This is the length of the unprocessed precursor]

Molecular weight: **59733 Da** [This is the MW of the unprocessed precursor]

CRC64: **E151372FF6C95BE7** [This is a checksum on the sequence]

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YCDADNNLEG	SLLN DIEEMK	TGYK DSPNLN	LIALVDRSPR	YSSDEKVLGE	DFSDTRLYKI
<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>
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REKSNPRLNR	AICWDDSNLD	KNGEADCLYM	GEISDHLTEK	QSVDLLAFDA	CLMGTAEVAY
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<u>490</u>	<u>500</u>	<u>510</u>	<u>520</u>		
NPYGKLSWCK	DGQDPEINKV	GNWFELLD SW	FDKTNDVTGG	VNHYQW	

P09870 in FASTA format

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or at NCBI (USA)




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Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)

ScanProsite, MotifScan

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File 444:New England Journal of Med. 1985-2005/Feb W1
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S2	4	S1 AND HISTOLYTICUM?
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2/9/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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09780560 PMID: 8341259

The heterodimeric protease clostripain from Clostridium histolyticum is encoded by a single gene.

Dargatz H ; Diefenthal T; Witte V; Reipen G; von Wettstein D

Weissheimer Research Laboratory, Andernach, Germany.

Molecular & general genetics - MGG (GERMANY) Jul 1993 , 240 (1)
p140-5, ISSN 0026-8925 Journal Code: 0125036

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Clostripain (EC 3.4.22.8) is a heterodimeric cysteine endopeptidase with strict specificity for Arg-Xaa peptidyl bonds. It is secreted by Clostridium histolyticum strains. For the first time we present evidence that both polypeptide chains of native clostripain are encoded by a single gene. DNA sequencing of two overlapping genomic DNA fragments revealed a single open reading frame (ORF) of 1581 nucleotides encoding a polypeptide of 526 amino acid residues. The ORF is preceded by canonical transcription signals and both chains of the clostripain heterodimer are completely represented by the deduced coding sequence. Most interestingly, the sequences coding for the light and the heavy chain are joined by a DNA stretch coding for a linker nonapeptide that is preceded by the C-terminal arginyl residue of the light chain and also ends with an arginyl residue. Heterologous expression of the gene in Escherichia coli yielded an enzyme capable of hydrolyzing the clostripain substrates N alpha-benzoyl-L-arginine ethyl ester (BAEE) and N-carbobenzoxy-L-arginine p-nitroanilide (Z-Arg-pNA).

Tags: Support, Non-U.S. Gov't

Descriptors: *Clostridium--enzymology--EN; *Cysteine Endopeptidases
--genetics--GE; *DNA, Bacterial--genetics--GE; *Genes, Bacterial--genetics
--GE; Amino Acid Sequence; Base Sequence; Clostridium--genetics--GE;
Cysteine Endopeptidases--isolation and purification--IP; Escherichia coli;
Gene Expression--genetics--GE; Molecular Sequence Data; Protein Sorting
Signals--genetics--GE; Transcription, Genetic--genetics--GE

Molecular Sequence Databank No.: GENBANK/X63673

CAS Registry No.: 0 (DNA, Bacterial); 0 (Protein Sorting Signals)

Enzyme No.: EC 3.4.22 (Cysteine Endopeptidases); EC 3.4.22.8
(clostripain)

Record Date Created: 19930902

Record Date Completed: 19930902